

GenCore version 5.1.4-p5_4578
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OM protein - protein search, using sw model

Run on: March 11, 2003, 23:09:45 ; Search time 53 Seconds
(without alignments)
2516.677 Million cell updates/sec

Title: US-10-046-433-40
Perfect score: 5506
Sequence: 1 MAEPGSHHLSARVRCRTER.....LGRSHNLPPRGLIMLTCR 1001

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues
Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: /SID2/gcgdata/geneseq/geneseq-emb1/AA1980.DAT.*
2: /SID2/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.*
3: /SID2/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.*
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21: /SID2/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
22: /SID2/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
23: /SID2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	5506	100.0	1001	22	AA835333
2	5376	97.6	1013	21	AA826179
3	5363	97.4	1013	22	AA83845
4	5341	97.0	1013	22	AA812190
5	5005	90.9	911	22	AA83850
6	4784	86.9	750	22	AA83851
7	3870	70.3	750	22	AA83328
8	2982.5	54.2	1027	22	AA870256
9	2815.5	51.1	963	22	AA870255
10	2491	45.2	495	20	AA859972

Result No.	Score	Query Match	Length	ID	Description
11	2119	38.5	383	22	AA83853
12	1761.5	32.0	372	22	AA85768
13	1448	26.3	464	22	AA848377
14	1307.5	23.7	411	22	AA848372
15	1169	21.2	209	22	AA83852
16	889.5	16.2	208	21	AA853442
17	776	14.1	147	22	AA83849
18	710	12.9	150	20	AA812274
19	518	9.4	105	21	AA826180
20	325	5.9	36	22	AA83847
21	284	5.2	74	22	AA870281
22	273	5.0	81	22	AA839918
23	273	5.0	81	22	AA824471
24	273	5.0	81	22	AA860663
25	273	5.0	81	22	AA873335
26	273	5.0	81	22	AA83355
27	273	5.0	81	23	AA843165
28	269	4.9	52	22	AA83848
29	252	4.6	1576	21	AA819802
30	252	4.6	1576	21	AA848453
31	252	4.6	1576	23	AA881595
32	252	4.6	1584	21	AA819804
33	252	4.6	1609	21	AA819801
34	252	4.6	1609	21	AA848452
35	252	4.6	1609	23	AA81594
36	252	4.6	1617	21	AA819803
37	251	4.6	1609	19	AA850898
38	244	4.4	45	22	AA83846
39	233	4.2	3594	23	AA820147
40	229.5	4.2	1572	21	AA819805
41	229.5	4.2	1572	21	AA848455
42	229.5	4.2	1572	23	AA881597
43	229.5	4.2	1605	21	AA819805
44	229.5	4.2	1605	21	AA848454
45	229.5	4.2	1605	23	AA881596

ALIGNMENTS

RESULT 1
ID: AA835333 standard; Protein: 1001 AA.
AA835333:
AC: AA835333:
XX: 08-MAY-2001 (first entry)
XX: 08-MAY-2001 (first entry)
XX: Human TR13 receptor protein SEQ ID NO: 40.
XX: Human; tumour necrosis factor receptor; TR13; TR14; infection;
XX: cancer; autoimmune disease; allergy; inflammatory disease;
XX: graft rejection; apoptosis; cardiovascular disease; aneurysm.
XX: OS
XX: Homo sapiens.
XX: W0200105834-AL.
XX: 25-JAN-2001.
XX: 14-JUL-2000; 2000WO-US19343.
XX: PF
XX: 16-JUL-1999; 99US-0144087.
XX: PR 18-AUG-1999; 99US-0149450.
XX: PR 20-AUG-1999; 99US-0149712.
XX: PR 10-SEP-1999; 99US-0153089.
XX: (HUMA-) HUMAN GENOME SCI INC.
XX: PA
XX: Ruben SM, Ni J, Young PE;
XX: PI
XX: WPI; 2001-112682/12.

PT Nucleic acids encoding 2 human tumor necrosis factor receptor
 PT polypeptides (TR13) and (TR14), useful for the prevention, diagnosis
 PT and treatment of, e.g. cancers, acquired immune deficiency syndrome and
 PT hypohidrotic ectodermal dysplasia -

XX Claim 40; Page 398-401; 418pp; English.

CC The present invention provides the protein and coding sequences of the
 CC human tumor necrosis factor receptors TR13 and TR14. These sequences are
 CC useful in the diagnosis and treatment of many diseases, including cancer,
 CC autoimmune diseases, cardiovascular disorders, allergies,
 CC neurodegenerative diseases, graft rejection, inflammation, aneurysms and
 CC infections.

XX Sequence 1001 AA;

Query Match 100.0%; Score 5506; DB 22; Length 1001;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1001; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAEPGSHHLSARVGRTERIPRLMRLLMAGTAFOVTOGTGPELHACKSEHYEYTA 60
 DB 1 MAEPGSHHLSARVGRTERIPRLMRLLMAGTAFOVTOGTGPELHACKSEHYEYTA 60
 QY 61 CDSTGSRMRVAVPHPTGICLSLPDPVKGTECSFSCNAGEFLDMKDQSCPKCAEGRYSLGT 120
 DB 61 CDSTGSRMRVAVPHPTGICLSLPDPVKGTECSFSCNAGEFLDMKDQSCPKCAEGRYSLGT 120
 QY 121 G1RFDEMDLPHGFASLSANMELDDSAESTNCTSKWVRGDIYANDECTATLMTYA 180
 DB 121 G1RFDEMDLPHGFASLSANMELDDSAESTNCTSKWVRGDIYANDECTATLMTYA 180
 QY 181 VNLKOSGTNFEYYPDSIIIEFFVQNDQCPNADSRMKTTEKGEFHSVELNNGN 240
 DB 181 VNLKOSGTNFEYYPDSIIIEFFVQNDQCPNADSRMKTTEKGEFHSVELNNGN 240
 QY 241 VLYNRTAFSVTKPKPVLVRLNITAGVATSCFPCKEPTYADKOGSSFCILCPANSTY 300
 DB 241 VLYNRTAFSVTKPKPVLVRLNITAGVATSCFPCKEPTYADKOGSSFCILCPANSTY 300
 QY 301 SSKGTSCHOCDDPKYSEKSSCNVRPACTDKDYFYTHACDANGETOIMTKMAKPKTC 360
 DB 301 SSKGTSCHOCDDPKYSEKSSCNVRPACTDKDYFYTHACDANGETOIMTKMAKPKTC 360
 QY 361 SEDLEGAVKLPAAGVKTCPKPCNPGFETKNNSTQPCPYGYSYNSGSDCTRCPAETPAVG 420
 DB 361 SEDLEGAVKLPAAGVKTCPKPCNPGFETKNNSTQPCPYGYSYNSGSDCTRCPAETPAVG 420
 QY 421 FEYKMWNTLPTNMEYTLVSGINEFYKGMTGMEVAGDHITTAAGASNDPMILTLVPGFR 480
 DB 421 FEYKMWNTLPTNMEYTLVSGINEFYKGMTGMEVAGDHITTAAGASNDPMILTLVPGFR 480
 QY 481 PROSVMDTEKKEVARTTFEFLICSYNCLYMGVNSRNTNPTVETWKGSGKGSYTYI 540
 DB 481 PROSVMDTEKKEVARTTFEFLICSYNCLYMGVNSRNTNPTVETWKGSGKGSYTYI 540
 QY 541 IEEYNTTSTFWAORTTFEHSRKYNDVAKIYSINVTVMVNGVASYCPCALAESDVGS 600
 DB 541 IEEYNTTSTFWAORTTFEHSRKYNDVAKIYSINVTVMVNGVASYCPCALAESDVGS 600
 QY 601 SCYSCPAGYIIDRDSGCHSCPNTILKAHOPGYQVACVPCGPGTKNNKIHSLCYNDCIF 660
 DB 601 SCYSCPAGYIIDRDSGCHSCPNTILKAHOPGYQVACVPCGPGTKNNKIHSLCYNDCIF 660
 QY 661 SRNPTTFENYNSALANTVTLAAGSPSTSKLAKYFHHHTLSLCNQGKMSVCTDNVTD 720
 DB 661 SRNPTTFENYNSALANTVTLAAGSPSTSKLAKYFHHHTLSLCNQGKMSVCTDNVTD 720
 QY 721 LRIPBESGFSKSTAYVQCAVILPEVYGYKAGVSSQPSVLADLILVTTDMLDGTGS 780
 DB 721 LRIPBESGFSKSTAYVQCAVILPEVYGYKAGVSSQPSVLADLILVTTDMLDGTGS 780
 QY 781 PALFLHESLGIIPDVIFFRSNDVYQSSGSGSTTIRVRCSPQKTVPGSLLLPCTSDGT 840

DB 781 PALFLHESLGIIPDVIFFRSNDVYQSSGSGSTTIRVRCSPQKTVPGSLLLPCTSDGT 840
 QY 841 CDGCFHFHWEESAACPLCSVADYHAIVSSCVAGICKTYYVREPKLCSGGSILPEQRYT 900
 DB 841 CDGCFHFHWEESAACPLCSVADYHAIVSSCVAGICKTYYVREPKLCSGGSILPEQRYT 900
 QY 901 ICKTIDFWLKVGISAGCTAIIITLVTCYFWKKNOKLEKYSKLVNMTLKKCDLPAADS 960
 DB 901 ICKTIDFWLKVGISAGCTAIIITLVTCYFWKKNOKLEKYSKLVNMTLKKCDLPAADS 960
 QY 961 CAIMEGEDVEDDILFTSKNHSIGRSNHLPPRGILMDLTQCR 1001
 DB 961 CAIMEGEDVEDDILFTSKNHSIGRSNHLPPRGILMDLTQCR 1001

RESULT 2
 AAB26179
 ID AAB26179 standard; Protein; 1013 AA.

AC AAB26179;
 DT 12-FEB-2001 (first entry)
 DE Human CASB619 protein #1.
 KW Human; CASB619; cancer; autoimmune disease; immunogen; vaccine;
 KW epitope.
 OS Homo sapiens.
 PN WO200058460-A2.
 PD 05-OCT-2000.
 XX 20-MAR-2000; 2000WO-EP02478.
 PF 26-MAR-1999; 99GB-00077113.
 PR 25-SEP-1999; 99GB-0022858.
 XX (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.

PI Bruck CEM, Cassart J, Coche T, Vinals De Bassols YC;
 XX WPI: 2000-664923/64.
 DR N-PSDB: AAA95442.
 XX Novel CASB619 polypeptides useful for diagnosing, and as vaccines for
 PT prophylactic and therapeutic treatment of, cancers, particularly
 PT ovarian and colon carcinoma, and autoimmune diseases -

PS Claim 4; Page 54-56; 68pp; English.
 CC The present sequence comprises the human CASB619 protein sequence. This
 CC protein is thought to be specifically or over-expressed in tumor cells,
 CC and so can be used as a target for antigen-specific immune responses
 CC which can cause destruction of the tumor cell. In addition, the protein
 CC and gene can be used in cancer diagnosis, in the treatment of autoimmune
 CC diseases and in vaccines against cancer and autoimmune disease. The
 CC invention provides a number of epitopes derived from the protein which
 CC can be used as immunogens.

XX Sequence 1013 AA;

Query Match 97.6%; Score 5376; DB 21; Length 1013;
 Best Local Similarity 99.4%; Pred. No. 0;
 Matches 978; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 MAEPGSHHLSARVGRTERIPRLMRLLMAGTAFOVTOGTGPELHACKSEHYEYTA 60
 DB 1 MAEPGSHHLSARVGRTERIPRLMRLLMAGTAFOVTOGTGPELHACKSEHYEYTA 60
 QY 61 CDSTGSRMRVAVPHPTGICLSLPDPVKGTECSFSCNAGEFLDMKDQSCPKCAEGRYSLGT 120

Db	61	CDSTGSRNRVAVHTTGLCTSLPDPVAKGTBCHSCNAAGEFLDMKDKSCAPCAEGRSLSLT	120
QY	121	GIRFDEWDELPHGFASIASANMELDDSAESTGNCSTSSKRVPRGDYIAFNTDECTATLMYA	180
Db	121	GIRFDEWDELPHGFASIASANMELDDSAESTGNCSTSSKRVPRGDYIASNTDECTATLMYA	180
QY	181	VNLKQSTVNFEXYYDPDSSIIEFFEPVONDDQCPNADSRMKTKTEKGWEPHVELNRGN	240
Db	181	VNLKQSTVNFEXYYDPDSSIIEFFEPVONDDQCPNADSRMKTKTEKGWEPHVELNRGN	240
QY	241	VLYWRTAFSVMTKVPKRPVLYRNIAITGVAYTSECEPPCKPGTYADKQGSFFCKLCPANSY	300
Db	241	VLYWRTAFSVMTKVPKRPVLYRNIAITGVAYTSECEPPCKPGTYADKQGSFFCKLCPANSY	300
QY	301	SNKGTSCHOCDDPKYSEKSSSCNRPACTDKDITYTHACHANGETQOLMYMAAPKTC	360
Db	301	SNKGTSCHOCDDPKYSEKSSSCNRPACTDKDITYTHACHANGETQOLMYMAAPKTC	360
QY	361	SEDEGAIVKLPASGVKTHCPNCPNGEFTKNNSTQPCPYSGYNGSDCTCPAGTEPAVG	420
Db	361	SEDEGAIVKLPASGVKTHCPNCPNGEFTKNNSTQPCPYSGYNGSDCTCPAGTEPAVG	420
QY	421	FEXKMWNTLPTNMETTVLSGINEEYKGMTEGVAAGDHIITYAAGASDNDFILTLVYVGR	480
Db	421	FEXKMWNTLPTNMETTVLSGINEEYKGMTEGVAAGDHIITYAAGASDNDFILTLVYVGR	480
QY	481	PROSVAMDTEKKEXARITTFPETFICSNCELYFVGVGNSSTNTPVETWKSCKGOSTYI	540
Db	481	PROSVAMDTEKKEXARITTFEETICSNCELYFVGVGNSKRTNTPVETWKSCKGOSTYI	540
QY	541	IEENNTTSFTWAFORTTFHEASRKTYTNDVAKIYSINVTNMGNGVASYCRPCALEASDVGS	600
Db	541	IEENNTTSFTWAFORTTFHEASRKTYTNDVAKIYSINVTNMGNGVASYCRPCALEASDVGS	600
QY	601	SCTSQCPAGYTYDRSGTCHSCPMTITLKAHOPVGVQACVPCGPETKNNKIHSILCYNDCTF	660
Db	601	SCTSQCPAGYTYDRSGTCHSCPMTITLKAHOPVGVQACVPCGPETKNNKIHSILCYNDCTF	660
QY	661	SRNPTRTFNFNFALSANTVYTLAAGPSFTSGKLYFHHFTLSLGCNQRKMSVCTDNVTD	720
Db	661	SRNPTRTFNFNFALSANTVYTLAAGPSFTSGKLYFHHFTLSLGCNQRKMSVCTDNVTD	720
QY	721	LRIPEGSEGSFKSTIAYVCOAVITIPPEYTGKKAIVSQPVSLADRLIGVTTDMTLDGITS	780
Db	721	LRIPEGSEGSFKSTIAYVCOAVITIPPEYTGKKAIVSQPVSLADRLIGVTTDMTLDGITS	780
QY	781	PAELFHELSLGIPIVIFPYFRANDVQSCSSRSTTIRKRCPOKRTVPGSLLPPTCSDGT	840
Db	781	PAELFHELSLGIPIVIFPYFRANDVQSCSSRSTTIRKRCPOKRTVPGSLLPPTCSDGT	840
QY	841	CDGCNHFHLMESAAAPCLCSYADYHAIYSSCVAGIOKTTYVWREPKILCSGSIIPBQRYT	900
Db	841	CDGCNHFHLMESAAAPCLCSYADYHAIYSSCVAGIOKTTYVWREPKILCSGSIIPBQRYT	900
QY	901	ICKTIDFPLKYGISGCTATILLVLTGYEPMKNOKLETXYKSKLYMNAATLKDCLPADS	960
Db	901	ICKTIDFPLKYGISGCTATILLVLTGYEPMKNOKLETXYKSKLYMNAATLKDCLPADS	960
QY	961	CAIMEGEVEDDLIFTSKNHSIGR 984	
Db	961	CAIMEGEVEDDLIFTSKNHSIGR 984	
RESULT 3			
AAB83845			
ID	AAB83845 standard; Protein: 1013 AA.		
XX			
AC	AAB83845;		
XX			
DT	23-JUL-2001 (first entry)		
Amino acid sequence of a human protein expressed in tumour cells.			

XX	Tumour cell; Immunological disease; autoimmune disease; cancer;
KV	infection.
XW	
OS	Homo sapiens.
XX	
FH	Key
FT	Location/Qualifiers
FT	Peptide
FT	1..41
FT	/note= "signal peptide"
FT	42..911
FT	/note= "extracellular domain"
FT	Domain
FT	912..930
FT	/note= "transmembrane domain"
FT	931..1013
FT	/note= "transmembrane domain"
XX	
PN	Domain
XX	
PD	WO200131003-AI.
PD	03-MAY-2001.
PF	30-OCT-2000; 2000WO-FR03032.
PR	
XX	29-OCT-1999; 99FR-0013629.
PA	(FABR) FABRE MEDICAMENT SA PIERRE.
XX	
PI	Delneste Y, Magistrelli G, Jeannin P, Bonnefoy J;
DR	WPI: 2001-328651/34.
N-PSDB:	AAF89765.
PT	New nucleic acid, expressed in tumours and lymphoid tissue is useful for
PT	identifying agents for treating tumours and autoimmune disease -
PS	Claim 9; Page 48-51; 85pp; French.
XX	
CC	The present sequence represents a human protein expressed in tumour
CC	cells. The polynucleotide is useful for screening cDNA/genomic DNA banks
CC	and for cloning isolated DNA; identifying mutant forms of the gene that
CC	encodes a human protein, where the mutations are associated with
CC	abnormal gene expression, or promoters and regulators of the gene,
CC	particularly for diagnosis; for recombinant expression of the derived
CC	protein; as probes and primers for detection and amplification; and
CC	as antisense therapeutics. The tumour expressed protein is useful for
CC	raising specific antibodies and to screen agents that modulate its
CC	activity, bind to it or interact with it. These agents are potentially
CC	useful for treatment or prevention of diseases associated with abnormal
CC	expression/activity of the protein, particularly immunological diseases
CC	(autoimmune diseases and cancer) or viral, bacterial, fungal or parasitic
CC	infections.
XX	
SQ	Sequence 1013 AA;
	Query Match 97.4%; Score 5363; DB 22; Length 1013;
	Best Local Similarity 99.2%; Pred. No. 0;
Matches 976;	Conservative 1; Mismatches 7; Indels 0; Gaps 0
QY	1 MAEPGSHSHLSARVGRTERRRIRLRLMLMAGTAQYVGTPPELHACKESSEYHYEXHA 60
DB	1 MAERGSHHSLSARVGRTERRRIRLRLMLMAGTAQYVGTPPELHACKESSEYHYEYTA 60
QY	61 CDGSGSWRAVAAPPTPLGLTSLPDPVYGTECSFCNNAGEFLDMKDCCKPCAGRYSLGT 120
DB	61 CDSGSGMWRAVAAPHTPLGLTSLPDPVYGTECSFCSCNNGEFLDMKDCCKPCAGRYSLGT 120
QY	121 GIRFDEWDELPHGFASISANMELDSDAESTGNCTSSKWVRGDYIAFNIDECAATLMYA 180
DB	121 GIRFDEWDELPHGFASISANMELDSDAESTGNCTSSKWVRGDYIASNTDECAATLMYA 180
QY	181 VNKKOSTVMPVEYYPPSSITFEFFVONDDCOPNADDSRMKKTTEKGMEFHSELNRGN 240
DB	181 VNLKOSTVMPVEYYPPSSITFEFFVONDDCOPNADDSRMKKTTEKGMEFHSELNRGN 240


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OY 1 MAEPGSHHLSARVGRTERIRIPRLMLLMAGTAFOVTOGTGPELHACKESYHEYYTA 60
DB 1 MAEPGSHHLSARVGRTERIRIPRLMLLMAGTAFOVTOGTGPELHACKESYHEYYTA 60
OY 61 CDSTGSRMRVAVPHPTPGICTSLPDPVKGTECSFSCNAGEFLDMKDDSCPCAGRYSLGT 120
DB 61 CDSTGSRMRVAVPHPTPGICTSLPDPVKGTECSFSCNAGEFLDMKDDSCPCAGRYSLGT 120
OY 121 GIREDEMDLPHGFASLSANMELDSDAESTGNTSSKWPVRDGYIAFNDECTATLMTA 180
DB 121 GIREDEMDLPHGFASLSANMELDSDAESTGNTSSKWPVRDGYIAFNDECTATLMTA 180
OY 181 VMLKOSGTVNFEXYYPDSIIIEFFVONDQCPNADDSRMWKTTEKMEFHSVELNRGN 240
DB 181 VMLKOSGTVNFEXYYPDSIIIEFFVONDQCPNADDSRMWKTTEKMEFHSVELNRGN 240
OY 241 VLYWRTAFSVWTKVPKPVLVNIAITGVATYSECPCPKGTADKOGSSFCILCPANSY 300
DB 241 VLYWRTAFSVWTKVPKPVLVNIAITGVATYSECPCPKGTADKOGSSFCILCPANSY 300
OY 301 SNKGETSCHQCDPKYSEKSSCNVRPACTDKDYEYHTACDANGETOIMTKAKPKIC 360
DB 301 SNKGETSCHQCDPKYSEKSSCNVRPACTDKDYEYHTACDANGETOIMTKAKPKIC 360
OY 361 SEDLEGAVKLPAAGVYTHCPNPGFETKNNSTCPCPYGYSNGSDCTRCPAGTEPAVG 420
DB 361 SEDLEGAVKLPAAGVYTHCPNPGFETKNNSTCPCPYGYSNGSDCTRCPAGTEPAVG 420
OY 421 FEYKMNNTLPJNMTTVLSGINFEYKMTGMVADHITYAAGSANDNFMLTLTVPEGR 480
DB 421 FEYKMNNTLPJNMTTVLSGINFEYKMTGMVADHITYAAGSANDNFMLTLTVPEGR 480
OY 481 PROSVADENKRVARTIEVETICVNCLELFMYGVNSRNTPYETKSGSKOSYTYI 540
DB 481 PROSVADENKRVARTIEVETICVNCLELFMYGVNSRNTPYETKSGSKOSYTYI 540
OY 541 IEENTTSPTWAFQRTTFHESAKRYNDVAKYISINVTVMNGVASYCPCPLEASDVGS 600
DB 541 IEENTTSPTWAFQRTTFHESAKRYNDVAKYISINVTVMNGVASYCPCPLEASDVGS 600
OY 601 SCTSCPAAGYIIDDSGCHSCPNTILKAHOPYGVACVPCPGFGRNNKIHSLCYNDCTF 660
DB 601 SCTSCPAAGYIIDDSGCHSCPNTILKAHOPYGVACVPCPGFGRNNKIHSLCYNDCTF 660
OY 661 SRNPTFTFVNFSAFLANTVTLAGPSFTSKGLYFHHFTLSLCGNOGRKMSVCTDNVTD 720
DB 661 SRNPTFTFVNFSAFLANTVTLAGPSFTSKGLYFHHFTLSLCGNOGRKMSVCTDNVTD 720
OY 721 LRIPEGESGESKSTAVVCAVVIIPREVTGYKAGVSSOPVSLADRLIGVTDMLDGTIS 780
DB 721 LRIPEGESGESKSTAVVCAVVIIPREVTGYKAGVSSOPVSLADRLIGVTDMLDGTIS 780
OY 781 PAELFHESLIGIPVIFEFYRSNDVTOSSSGRSTTIVRCSPOKTVPGSILLEGTSDDCT 840
DB 781 PAELFHESLIGIPVIFEFYRSNDVTOSSSGRSTTIVRCSPOKTVPGSILLEGTSDDCT 840
OY 841 CDGCFHFLIMESAACPLCSVADYHAIVSSCVAGIQKTTYVWREPKLCSGSLSPORAT 900
DB 841 CDGCFHFLIMESAACPLCSVADYHAIVSSCVAGIQKTTYVWREPKLCSGSLSPORAT 900
OY 901 ICKTIDFMLKYGISAGTCTALLVLCYFPWKNOULEYKSKLYMNAATLKDCLPAADS 960
DB 901 ICKTIDFMLKYGISAGTCTALLVLCYFPWKNOULEYKSKLYMNAATLKDCLPAADS 960
OY 961 CAIMEGEDEVEDLIFTSKNHSIGR 984
DB 961 CAIMEGEDEVEDLIFTSKNHSIGR 984

```

RESULT 5
AAB83850
AAB83850 standard; Protein; 911 AA.

```

XX AAB83850;
AC 23-JUL-2001 (first entry)
DE Amino acid sequence of a human protein expressed in tumour cells.
KW Tumour cell; immunological disease; autoimmune disease; cancer;
OS infection.
XX Homo sapiens.
XX WO200131003-A1.
XX 03-MAY-2001.
XX 30-OCT-2000; 2000WO-FR03032.
XX 29-OCT-1999; 99FR-0013629.
XX (FABR ) FABRE MEDICAMENT SA PIERRE.
XX Delneste Y, Magistrelli G, Jeannin P, Bonnefoy J;
XX WPI: 2001-328651/34.
XX N-PSDB: AAF89774.
XX New nucleic acid, expressed in tumours and lymphoid tissue is useful for
XX identifying agents for treating tumours and autoimmune disease
XX Claim 10; Page 60-63; 85pp; French.
XX
XX The present sequence represents a human protein expressed in tumour
XX cells. The polynucleotide is useful for screening cDNA/genomic DNA banks
XX and for cloning isolated DNA; identifying mutant forms of the gene that
XX encodes a human protein, where the mutations are associated with
XX abnormal gene expression, or promoters and regulators of the gene,
XX particularly for diagnosis; for recombinant expression and amplification; and
XX protein; as probes and primers for detection and amplification; and
XX as antisense therapeutics. The tumour expressed protein is useful for
XX raising specific antibodies and to screen agents that modulate its
XX activity, bind to it or interact with it. These agents are potentially
XX useful for treatment or prevention of diseases associated with abnormal
XX expression/activity of the protein, particularly immunological diseases
XX (autoimmune diseases and cancer) or viral, bacterial, fungal or parasitic
XX infections.
XX
XX Sequence 911 AA:
XX
XX Query Match 90.9%; Score 5005; DB 22; Length 911;
XX Best Local Similarity 99.7%; Pred. No. 0;
XX Matches 908; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
OY 1 MAEPGSHHLSARVGRTERIRIPRLMLLMAGTAFOVTOGTGPELHACKESYHEYYTA 60
DB 1 MAEPGSHHLSARVGRTERIRIPRLMLLMAGTAFOVTOGTGPELHACKESYHEYYTA 60
OY 61 CDSTGSRMRVAVPHPTPGICTSLPDPVKGTECSFSCNAGEFLDMKDDSCPCAGRYSLGT 120
DB 61 CDSTGSRMRVAVPHPTPGICTSLPDPVKGTECSFSCNAGEFLDMKDDSCPCAGRYSLGT 120
OY 121 GIREDEMDLPHGFASLSANMELDSDAESTGNTSSKWPVRDGYIAFNDECTATLMTA 180
DB 121 GIREDEMDLPHGFASLSANMELDSDAESTGNTSSKWPVRDGYIAFNDECTATLMTA 180
OY 181 VMLKOSGTVNFEXYYPDSIIIEFFVONDQCPNADDSRMWKTTEKMEFHSVELNRGN 240
DB 181 VMLKOSGTVNFEXYYPDSIIIEFFVONDQCPNADDSRMWKTTEKMEFHSVELNRGN 240
OY 241 VLYWRTAFSVWTKVPKPVLVNIAITGVATYSECPCPKGTADKOGSSFCILCPANSY 300
DB 241 VLYWRTAFSVWTKVPKPVLVNIAITGVATYSECPCPKGTADKOGSSFCILCPANSY 300

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OY 301 SNKGETSCHODDPKYSKSSSCNVBPACTDKDYFTHHACDANGETOIMYKAPKIC 360
DB 301 SNKGETSCHODDPKYSKSSSCNVBPACTDKDYFTHHACDANGETOIMYKAPKIC 360
OY 361 SEDLEGAVKLAASGVKTHCPNCPNPGFKTNNSTQCPCPYGSYNSGSDCTFCAPGTEPAVG 420
DB 361 SEDLEGAVKLAASGVKTHCPNCPNPGFKTNNSTQCPCPYGSYNSGSDCTFCAPGTEPAVG 420
OY 421 FEYKMMNTLPNTMETVYLSGINFEXKGMTGMEVAGDHITAAASNDNDMLLVVPGFR 480
DB 421 FEYKMMNTLPNTMETVYLSGINFEXKGMTGMEVAGDHITAAASNDNDMLLVVPGFR 480
OY 481 PROSVADTEKKEVARITFEVETLCSVNCLELYPMGVNSRTNTPVETWKGSGKOSYTYI 540
DB 481 PROSVADTEKKEVARITFEVETLCSVNCLELYPMGVNSRTNTPVETWKGSGKOSYTYI 540
OY 541 IEENTTSFTWAFORTFHEASRKYNDVAKIYSINVTVMNGVASYCRPCALEASDVGS 600
DB 541 IEENTTSFTWAFORTFHEASRKYNDVAKIYSINVTVMNGVASYCRPCALEASDVGS 600
OY 601 SCTSCPAGYIIDRSGTCHSCPNTILKAHOPGYQACVPGPGRKNNKIHSLCYNDCGF 660
DB 601 SCTSCPAGYIIDRSGTCHSCPNTILKAHOPGYQACVPGPGRKNNKIHSLCYNDCGF 660
OY 661 SRMTPTFTFNFNSALANTVTLAGSPFTSKGLKFHHFTLSLCSNCGKMSVCTDNVTD 720
DB 661 SRMTPTFTFNFNSALANTVTLAGSPFTSKGLKFHHFTLSLCSNCGKMSVCTDNVTD 720
OY 721 LRIPESGFSKSTAYVCOAVIIPPEVGYKAGVSSOPVSLADLLIVTDMTLDTGTS 780
DB 721 LRIPESGFSKSTAYVCOAVIIPPEVGYKAGVSSOPVSLADLLIVTDMTLDTGTS 780
OY 781 PALFLESLGIDVYEFRRSDVYQSCSGSTTIRVRCSPQKTVPGLLPCTCSDGT 840
DB 781 PALFLESLGIDVYEFRRSDVYQSCSGSTTIRVRCSPQKTVPGLLPCTCSDGT 840
OY 841 CDGCFHFLMESAAACPLCSVADYHAIVSSCVAGIOKTTYVWREPKLCSGSIPEQRYT 900
DB 841 CDGCFHFLMESAAACPLCSVADYHAIVSSCVAGIOKTTYVWREPKLCSGSIPEQRYT 900
OY 901 ICKTIDFWLKV 911
DB 901 ICKTIDFWLKV 911

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RESULT 6
AAB83851
ID AAB83851 standard; Protein: 870 AA.
XX
AC AAB83851;
XX
DT 23-JUL-2001 (first entry)
XX
DE Amino acid sequence of a human protein expressed in tumour cells.
XX
KW Tumour cell; immunological disease; autoimmune disease; cancer;
XX
KW Infection.
XX
OS Homo sapiens.
XX
PN MO200131003-A1.
XX
PD 03-MAY-2001.
XX
PF 30-OCT-2000; 2000MO-FR03032.
XX
PR 29-OCT-1999; 99PR-0013629.
XX
PA (FABR) FABRE MEDICAMENT SA PIERRE.
XX
PI Delneste Y, Magistrelli G, Jeannin P, Bonnefoy J;
XX
DR WPI; 2001-328651/34.

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DR N-PSDB: AAF89775.
XX
PT New nucleic acid, expressed in tumours and lymphoid tissue is useful for
PT Identifying agents for treating tumours and autoimmune disease
XX
PS Claim 10; Page 67-70; 85pp; French.
XX
CC The present sequence represents a human protein expressed in tumour
CC cells. The polynucleotide is useful for screening cDNA/genomic DNA banks
CC and for cloning isolated DNA; identifying mutant forms of the gene that
CC encodes a human protein, where the mutations are associated with
CC abnormal gene expression, or promoters and regulators of the gene,
CC particularly for diagnosis; for recombinant expression and amplification; and
CC as antisense therapeutics. The tumour expressed protein is useful for
CC raising specific antibodies and to screen agents that modulate its
CC activity, bind to it or interact with it. These agents are potentially
CC useful for treatment or prevention of diseases associated with abnormal
CC expression/activity of the protein, particularly immunological diseases
CC (autoimmune diseases and cancer) or viral, bacterial, fungal or parasitic
CC infections.
XX
XX
Sequence 870 AA:
Query Match 86.9%; Score 4784; DB 22; Length 870;
Best local Similarity 99.7%; Pred. No. 0;
Matches 867; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
OY 42 TGBELHACKESEHYEYACDSTGSRMRVAVPHFGICTSLPDPVKGECFSCNAGEFL 101
DB 1 TGBELHACKESEHYEYACDSTGSRMRVAVPHFGICTSLPDPVKGECFSCNAGEFL 60
OY 102 DMKDSCRCACAGRSISLGTGIRFDEMDLPHGFASLSANMELDASAESTGNCSTSKWP 161
DB 61 DMKDSCRCACAGRSISLGTGIRFDEMDLPHGFASLSANMELDASAESTGNCSTSKWP 120
OY 162 RGDYIAFNTDECTATAMAVNLKOSGTNFEYYPDSISIFEEFVQNDCCOPNADSRM 221
DB 121 RGDYIAFNTDECTATAMAVNLKOSGTNFEYYPDSISIFEEFVQNDCCOPNADSRM 180
OY 222 KTEKGWGFHSEYELRGNVLYWRTAFSVWTKVPRVLRNIAITGVATSECFPCRQ 281
DB 181 KTEKGWGFHSEYELRGNVLYWRTAFSVWTKVPRVLRNIAITGVATSECFPCRQ 240
OY 282 TYADKQSSFPCKLCPANSYKNGFTSCHODDPKYSKSSSCNVBPACTDKDYFTHH 341
DB 241 TYADKQSSFPCKLCPANSYKNGFTSCHODDPKYSKSSSCNVBPACTDKDYFTHH 300
OY 342 CDANGETOIMYKAPKICSEDELGAVKLPASGVKTHCPNCPNPGFKTNNSTQCPCPYGS 401
DB 301 CDANGETOIMYKAPKICSEDELGAVKLPASGVKTHCPNCPNPGFKTNNSTQCPCPYGS 360
OY 402 YSNGSDCTRCPCAGTEPAVGFYKMMNTLPNTMETVYLSGINFEXKGMTGMEVAGDHIT 461
DB 361 YSNGSDCTRCPCAGTEPAVGFYKMMNTLPNTMETVYLSGINFEXKGMTGMEVAGDHIT 420
OY 462 AGASDNDFMILLVVPGRPOSVMADEKKEVARITFEVETLCSVNCLELYPMGVNSRT 521
DB 421 AGASDNDFMILLVVPGRPOSVMADEKKEVARITFEVETLCSVNCLELYPMGVNSRT 480
OY 522 NTPVETWKGSGKOSYTYIIEENTTSFTWAFORTFHEASRKYNDVAKIYSINVTVM 581
DB 481 NTPVETWKGSGKOSYTYIIEENTTSFTWAFORTFHEASRKYNDVAKIYSINVTVM 540
OY 582 NGVASYCRPCALASDVGSCTCPAGYIIDRSGTCHSCPNTILKAHOPGYQACVPC 641
DB 541 NGVASYCRPCALASDVGSCTCPAGYIIDRSGTCHSCPNTILKAHOPGYQACVPC 600
OY 642 GPGTKNNKIHSLCYNDCFTSRNTPFTFNFNSALANTVTLAGSPFTSKGLKFHHFTL 701
DB 601 GPGTKNNKIHSLCYNDCFTSRNTPFTFNFNSALANTVTLAGSPFTSKGLKFHHFTL 660
OY 702 SLCSNCGKMSVCTDNVTDLRIPESGFSKSTAYVCOAVIIPPEVGYKAGVSSOPVS 761

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Db 661 SLGNGRKMSEVCTDNDVTLRIPEGESEFSKSTIAYVQAVIIPPEVTGKAAVSQPS 720
QY 762 LADRLIGVTTMTLDGITSIPAELFHELSIGIPDIYFFYRSDNYTQSSSGRSTTIRVCS 821
Db 721 LADRLIGVTTMTLDGITSIPAELFHELSIGIPDIYFFYRSDNYTQSSSGRSTTIRVCS 780
QY 822 POKTVPGSLLPPTGSDGTCDGCFNHFLESAACPLCSVADYHAIYSSCVAGIQTYY 881
Db 781 POKTVPGSLLPPTGSDGTCDGCFNHFLESAACPLCSVADYHAIYSSCVAGIQTYY 840
QY 882 WREPILCSGIGISLPQORVITCKTIDFWLKV 911
Db 841 WREPILCSGIGISLPQORVITCKTIDFWLKV 870

RESULT 7
AAB35328
ID AAB35328 standard; protein; 750 AA.
XX
AC AAB35328;
XX
DT 08-MAY-2001 (first entry)
XX
DE Human TR13 receptor protein SEQ ID NO: 2.
XX
KW Human; tumour necrosis factor receptor; TR13; TR14; infection;
KW cancer; autoimmune disease; allergy; inflammatory disease;
KW graft rejection; apoptosis; cardiovascular disease; aneurysm.
XX
OS Homo sapiens.
XX
FN WO200105834-A1.
XX
PD 25-JAN-2001.
XX
PF 14-JUL-2000; 2000WO-US19343.
XX
PR 16-JUL-1999; 99US-0144087.
PR 18-AUG-1999; 99US-0149450.
PR 20-AUG-1999; 99US-0149712.
PR 10-SEP-1999; 99US-0153089.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Ruben SM, Ni J, Young PE;
XX
DR WPI; 2001-112682/12.
XX
N-PSDB; AAF27997.
XX
PT Nucleic acids encoding 2 human tumor necrosis factor receptor
PT polypeptides ((TR13) and (TR14)), useful for the prevention, diagnosis
PT and treatment of, e.g. cancers, acquired immune deficiency syndrome and
PT hypohidrotic ectodermal dysplasia -
XX
PS Claim 40; Page 369-372; 418pp; English.
XX
CC The present invention provides the protein and coding sequences of the
CC human tumour necrosis factor receptors TR13 and TR14. These sequences are
CC useful in the diagnosis and treatment of many diseases, including cancer,
CC autoimmune diseases, cardiovascular disorders, allergies,
CC neurodegenerative diseases, graft rejection, inflammation, aneurysms and
CC infections.
XX
SQ Sequence 750 AA;
XX
Query Match 70.3%; Score 3870; DB 22; Length 750;
Best Local Similarity 99.0%; Pred. No. 1.6e-293;
Matches 707; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 288 GSSFECKLCPAASVSNKGETSCHODDPDKYSEKSSSCNVPACTDMDYFYTHTACDANCE 347
Db 37 GILFLQTLPSNSYNKGETSCHODDPDKYSEKSSSCNVPACTDMDYFYTHTACDANCE 96

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QY 348 TOLMYKNAKPKICSEDELEGAVKLPASGVKTHCPNCPNGFFKTNNSTQCOPCYGSGSNGSD 407
Db 97 TOLMYKNAKPKICSEDELEGAVKLPASGVKTHCPNCPNGFFKTNNSTQCOPCYGSGSNGSD 156
QY 408 CTRCPAGTEPVAEVEYKWMNTLPTNMETTVLSGINFEEYKMTGQNEVAGDHITTAAGASDN 467
Db 157 CTRCPAGTEPVAEVEYKWMNTLPTNMETTVLSGINFEEYKMTGQNEVAGDHITTAAGASDN 216
QY 468 DEMILTLVPGFRPQSVMAOTENKEVARITFEVETLCSVNCLELYFWAGVNSRFTNPVET 527
Db 217 DEMILTLVPGFRPQSVMAOTENKEVARITFEVETLCSVNCLELYFWAGVNSRFTNPVET 276
QY 528 WKSGKSGKSYTYIIEENTTSFTNAFQRTTFEASRKYNDVAKYISINTNVNNGASY 587
Db 277 WKSGKSGKSYTYIIEENTTSFTNAFQRTTFEASRKYNDVAKYISINTNVNNGASY 336
QY 588 CRPCALEASDVSSCTSCPAGYIDRDSGTCHSCPNTILKAHOPYQVQACVPCGPGTKN 647
Db 337 CRPCALEASDVSSCTSCPAGYIDRDSGTCHSCPNTILKAHOPYQVQACVPCGPGTKN 396
QY 648 NKIHSLCYNDCTFSRNTPTRTFNYSALANTVTLAGGSFTSKGLKYFHHFTLSLGNQ 707
Db 397 NKIHSLCYNDCTFSRNTPTRTFNYSALANTVTLAGGSFTSKGLKYFHHFTLSLGNQ 456
QY 708 GRKMSVCTDNDVTLRIPEGESEFSKSTIAYVQAVIIPPEVTGKAAVSQPSIADRLI 767
Db 457 GRKMSVCTDNDVTLRIPEGESEFSKSTIAYVQAVIIPPEVTGKAAVSQPSIADRLI 516
QY 768 GVTTDMTLDGITSIPAELFHELSIGIPDIYFFYRSDNYTQSSSGRSTTIRVCSPOKTV 827
Db 517 GVTTDMTLDGITSIPAELFHELSIGIPDIYFFYRSDNYTQSSSGRSTTIRVCSPOKTV 576
QY 828 GSLLPPTGSDGTCDGCFNHFLESAACPLCSVADYHAIYSSCVAGIQTYYWREPIL 887
Db 577 GSLLPPTGSDGTCDGCFNHFLESAACPLCSVADYHAIYSSCVAGIQTYYWREPIL 636
QY 888 CSGSISLPQORVITCKTIDFWLKVISAGRTAIIILTVLTCYFMKNOKLEXYSKLVAN 947
Db 637 CSGSISLPQORVITCKTIDFWLKVISAGRTAIIILTVLTCYFMKNOKLEXYSKLVAN 696
QY 948 ATKDKCDLPADSCAIMEGEDEDDLIFTSKNHSLSGNSHLPRGLIMDLTOCR 1001
Db 697 ATKDKCDLPADSCAIMEGEDEDDLIFTSKNHSLSGNSHLPRGLIMDLTOCR 750

RESULT 8
AAB70256
ID AAB70256 standard; protein; 1027 AA.
XX
AC AAB70256;
XX
DT 10-MAY-2001 (first entry)
XX
DE TR16-long receptor protein.
XX
KW TR16 receptor; tumour necrosis factor receptor superfamily;
KW apoptosis; inflammatory; cancer; immune; neurodegenerative.
XX
OS unidentified.
XX
FN WO200112671-A1.
XX
PD 22-FEB-2001.
XX
PF 10-AUG-2000; 2000WO-US21885.
XX
PR 12-AUG-1999; 99US-0148348.
PR 13-AUG-1999; 99US-0148683.
PR 13-AUG-1999; 99US-0148670.
PR 16-AUG-1999; 99US-0148758.
PR 17-AUG-1999; 99US-0149181.
PR 18-AUG-1999; 99US-0149453.

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PR 19-AUG-1999; 9905-0149498.
 XX (HUMA-) HUMAN GENOME SCI INC.
 PA
 PI Ruben SM, Young PE, Baker KP;
 XX WPI; 2001-138754/14.
 DR
 XX
 PT New nucleic acid molecule encoding a TR16 tumor necrosis factor
 PT receptor polypeptide, useful for the diagnosis and treatment of cancer,
 PT autoimmune disorders and cardiovascular diseases -
 XX
 PS Disclosure; Fig 4; 286pp; English.
 CC
 CC The present invention relates to a TR16 receptor (tumour necrosis
 CC factor receptor superfamily). The invention is useful treating
 CC diseases and disorders associated with the inhibited or increased
 CC apoptosis. In particular inflammatory diseases, cancers, immune and
 CC neurodegenerative disorders may be treated.
 XX
 SQ Sequence 1027 AA;

Query Match 54.2%; Score 2982.5; DB 22; Length 1027;
 Best Local Similarity 53.6%; Pred. No. 1.7e-225;
 Matches 530; Conservative 168; Mismatches 270; Indels 21; Gaps 11;

OY 15 RGRTERRIIPR---LMRL---LWAGTAFOYTGTEGPELHACKSEHYHYETACDSTGSR 67
 DB 23 RGRSPSPAMICWALAGCOAAMAG--DLPSSSRPLPPCQKDYHFEYTCDDSSGSR 79
 OY 68 WRVAVPHTPGICTSLPDPVKGTSCSFSCNAGEFLDMKDCCKPCAREYSLGIGIFEDW 127
 DB 80 WRVAVPNSAVVDCSGLPDPVRGKECTFCASGEYIEKMNQVCSKGBETSLGSGIFEDW 139
 OY 128 DELPHGFASLSANNELDSDAAS-TCNCTSSKVPYRGDTAFTNIDCTATLMAVNLKOS 186
 DB 140 DELPAGSNNITFMDTVVGBSDSRPDGNNNSWIPRGNTIESNRDCTSLIYAVHLKKS 199
 OY 187 GTVNFEEYYPDSIIPEFVQNDQCP-NADDSRMKTEKNG-NEHSHSELNKNVNLW 244
 DB 200 GYVFEFYQYVNNIIEFFFIQNDQCEMDITTKWKVLTNDGEMGSHSLKSGNIIW 259
 OY 245 RTTAFSVWTKVPRVLYRNATITGAVTSECFPCPGTYADRGSSFCILCPANSYNGK 304
 DB 260 RTTGILMGSAVRPVLYKNTTIGVAVTSECFPCPGTFSNKGPSNQCVCRRNTYSEK 319
 OY 305 ETSCHOC-DEPKYSEKSSCNRPACTDKDYFTHTADANGETQIMAKKPRICSD 363
 DB 320 AKECIRCKDSDQS--GSSECTERPECTTKDYFQIHTPCDEGKTQIMYKWIPEKICRED 377
 OY 364 LBGAVLPLASGYKTHCPCNPGFFKTNSTCQPCPYGSYSNGS-DCTRCPAGTEPAVFE 422
 DB 378 LQDAIRLPPSGEKKDCPCNPGFYNNSSSCHPCPGTFSODTKRCRCRCPAGTEPALFE 437
 OY 423 YKMMNTLPNNMETVLSGINFEXKMTGEVAGDHIYTAAGASDNDMLLVVGPFRP 482
 DB 438 YKMMNTLPNNMTSCFNNNGNSKCDGMNGEWAAGDIOGAGSDNDYLILMLHPGRKP 497
 OY 483 OSVAMDTENKEVARTTVEFTLCVNCLELYPMGVNSTNTPVETWNGSKGOSYTIIE 542
 DB 498 TS-MGATGSEELGITTFEFTLCADCVLYFVNDINKSTVWVSWGTEKQAYTHIF 556
 OY 543 EMTTSTFMARORTTFHASKRTYNDVAKIYSIVNTVMNGVASYCPALASDVSSC 602
 DB 557 KNAITTFMARORINOGDNRFRINDVAKIYSINATNAVGVASSACALGSEQSSSC 616
 OY 603 TSCPAGYIDRSGTCHSCPNTITLKAHOPAGVACPCPRKNNKTHSLCINDCTFSR 662
 DB 617 VPCPGHYIEKETNOCKKCPDYTLISHOYKACACIPCGPCKNNQDHSVCSDCFYH 676
 OY 663 NTPRTFYNNSALANVTYLAGSPSTSKIKYFHHTFTSLCNGQKSKSVCTDNTDTR 722
 DB 677 EKENOILHYDESNLSVSGILMNGSPSTSKIKYFHHTFTSLCNGHKKMAALCTNNITDFT 736

OY 723 IPE---GSEGSKSITAYVQAVIIPPEVYTKAGVSSQPSVLADRLIGVTTMDLDCIT 779
 DB 737 KVELVAGSDRYTLVGVAFVQOSTIPSESKGFRALSSOSIILADTFIGVFEYETLKNIN 796
 OY 780 SPAELHLESIGIPDIVIFEYRSNDVYQSCSSGRSTTIRVCSPOKTPVSGILLPOTCSDG 839
 DB 797 IKEDMFPVPTSQLPDVHFEYKSTATTSCINGRSTAVAKRCPTKSGAGVLSVPSKCPAG 856
 OY 840 TCDGCFHFLWESAACPLCSADVADHAIVSSCVAGIQTKTYVMREPKLSGSGISLPEQRY 899
 DB 857 TCDGCTFTFLWESAACPLCTEDHEIEGACKRGFOETLYVMNEPKVICIGISLPEKIL 916
 OY 900 TICKTIDFWLKVGISAGTCTAILTLVLCYFPKKNKLEKYYSKLVNMTATKDCDLPAD 939
 DB 917 ANCEVDFVFLKVGAGVAFATVLAALCYTRKKNQKLEIKSLVMTJNSKECELPAD 976
 OY 960 SCALMEGEVEEDLFTSKNSLSGRSNHL 988
 DB 977 SCALMEGEDNEEEVYVSNKOSILGKLKSL 1005

RESULT 9
 AAB70255
 ID AAB70255 standard; protein; 963 AA.
 XX
 AC AAB70255;
 XX
 DT 10-MAY-2001 (first entry)
 DE
 DE TR16-short receptor protein.
 XX
 KW TR16 receptor; tumour necrosis factor receptor superfamily;
 KW apoptosis; inflammatory; cancer; immune; neurodegenerative.
 XX
 OS Unidentified.
 XX
 PN WO200112671-A1.
 PD
 PD 22-FEB-2001.
 XX
 PF 10-AUG-2000; 2000MO-US21885.
 XX
 PR 12-AUG-1999; 9905-0148348.
 PR 13-AUG-1999; 9905-0148683.
 PR 16-AUG-1999; 9905-0148870.
 PR 17-AUG-1999; 9905-0148758.
 PR 18-AUG-1999; 9905-0149181.
 PR 19-AUG-1999; 9905-0149453.
 XX
 XX (HUMA-) HUMAN GENOME SCI INC.
 PA
 PI Ruben SM, Young PE, Baker KP;
 XX WPI; 2001-138754/14.
 XX

New nucleic acid molecule encoding a TR16 tumor necrosis factor
 PT receptor polypeptide, useful for the diagnosis and treatment of cancer,
 PT autoimmune disorders and cardiovascular diseases -
 XX
 PS Claim 1; Fig 1; 286pp; English.

The present invention relates to a TR16 receptor (tumour necrosis
 CC factor receptor superfamily). The invention is useful treating
 CC diseases and disorders associated with the inhibited or increased
 CC apoptosis. In particular inflammatory diseases, cancers, immune and
 CC neurodegenerative disorders may be treated.
 XX

Query Match 51.1%; Score 2815.5; DB 22; Length 963;
 Best Local Similarity 52.8%; Pred. No. 2.2e-212;

Matches	501; Conservative	161; Mismatches	261; Indels	25; Gaps	12;
OY	15 RGRTERIR---LRL-----LMAAGTAFOYVYOGTGPFLHACKSESEVYEXTACDSTGSR	67			
DB	23 RGRSPWSPAMICCMALACQAMAG---DLPSSSRLPPOCKEDYFEFTECDSSGR	79			
OY	68 WRAVAHPHTGLTSLPDPAKGTGECSPSCNAGEFLDMKDQSKPCAEGRYSIGTGIRPEW	127			
DB	80 WRAVAIRSAVDCGLPDVPRKKECTFSCASGELEKMKQVSKCEGTYSLSGSGIKPEW	139			
OY	128 DELPHGASISANMELDDSAES--TGNCSSKRVPRGDIATFNTDECTATIMAYANLKS	186			
DB	140 DELPAGSNATFMDTVVPGSDSPDGKNNSSWIPRGNTIESNRDCTISLIYANHLKS	199			
OY	187 GTVAFEEYDDSSIIFFEFVONDOP--NADDSRMKKTTEK--WEFHSVELRNKNNLYW	244			
DB	200 GYVEFEYQYDNNITFEFFIIONDQCEMDTDTDKVYKLDNGEMGSHVLMKSGTNILY	259			
OY	245 RTTAFSVTKVPKPVLRNIAITGVATSCFPCPKGTADKQSSFCCLCPANSYNG	304			
DB	260 RTTGILMSKAVKPVLRNITIEGVAATSCFPCPKGTADKQSSFCCLCPANSYNG	319			
OY	305 ETSCHOC--DPDKYSEKSSSCNVPACTDKDYTYHTACDANGETOLMKAKPKICSD	363			
DB	320 AKECIRCKDSDSFS--GSSECTERPTCTDYQIHTPCDEEGKTOIMYKWIPEKICRD	377			
OY	364 LEGAVKLPASGVKTHPCPCNPGFRTKNNSTOCPCPYSGSNGS--DCTCPAGTEPAVGE	422			
DB	378 LTDAIRLPSPGEKKKPCPCNPGFRTKNNSTOCPCPYSGSNGS--DCTCPAGTEPAVGE	437			
OY	423 YKMMNLTLPNNMTYVLSINFYKMGMEVAGDHIYAGAANDMILLTVVPGFRP	482			
DB	438 YKMMNLTLPNNMTYVLSINFYKMGMEVAGDHIYAGAANDMILLTVVPGFRP	497			
OY	483 OSVADTENKEVARITFEVETLCYNCLYFMGVNKNSTNPTVPMWGSKQKOSTYIE	542			
DB	498 TS--MTGATSELRITFEVETLCYNCLYFMGVNKNSTNPTVPMWGSKQKOSTYIE	556			
OY	543 ENRTTFMFAQRTFHEASRYTNDVAKIYSINVTNMGVASYRCPCALEASDVSSC	602			
DB	557 KNTTFMFAQRTFHEASRYTNDVAKIYSINVTNMGVASYRCPCALEASDVSSC	616			
OY	603 TSCPAGYIDRSGTCHSCPNTILKAHPYVOVQACGCPETKNNKTHSICYNDCPSR	662			
DB	617 VPCPGYIDRSGTCHSCPNTILKAHPYVOVQACGCPETKNNKTHSICYNDCPSR	676			
OY	663 NTPEPTFNYSALANTVTLAGSPSTSGKLYFHHFTLSLGNQGRKMSVCTDNDLR	722			
DB	677 EKENDIHFPSNLSVSGSLMNGPSTSGKLYFHHFTLSLGNQGRKMSVCTDNDLR	736			
OY	723 IPE---GESGFSKITAAYCOAVIIPPEYTGKAGYSSOPVSLADRLIGVTTDMTLDGIT	779			
DB	737 VKELVAGSDYTNLVCAGFOQSTIIPSESGKFRALSSOSIILADFLIYVETILKNIN	796			
OY	780 SPALFHELSGIPDVIFEYFRSNDVQSCSSGRSTIRVRCSPQKTPVPSLLPGTCSG	839			
DB	797 IKEMFEPVPSQIPDVIFEYFRSNDVQSCSSGRSTIRVRCSPQKTPVPSLLPGTCSG	856			
OY	840 TDCGNEHFLWESAACPLCSVADYDAIVSSCAVAGIOKTYVWRREKLISGGISLEQRY	899			
DB	857 TDCGNEHFLWESAACPLCSVADYDAIVSSCAVAGIOKTYVWRREKLISGGISLEQRY	916			
OY	900 TICTKIDFWLVAGISAGCTAIIITLVLCYFMKKNQKYLEYKSKLVYN	947			
DB	917 ATCEIVDFWLVAGISAGCTAIIITLVLCYFMKKNQKYLEYKSKLVYN	960			

RESULT 10
AA59972
ID AA59972 standard; Protein: 495 AA.
XX
AC
XX
AA59972;
XX

DT	31-JAN-2000 (first entry)	
XX		
DE	Human endometrium tumour EST encoded protein 32.	
XX		
KW	Endometrium; human; tumour; cancer; anticancer; cytostatic; EST;	
KW	treatment; uterine; gene therapy; expressed sequence tag.	
XX		
OS	Homo sapiens.	
XX		
PN	DE19817948-A1.	
XX		
PD	21-OCT-1999.	
XX		
PF	17-APR-1998; 98DE-1017948.	
XX		
PR	17-APR-1998; 98DE-1017948.	
XX		
PA	(META-) METAGEN GES GENOMFORSCHUNG MBH.	
XX		
PI	Rosenthal A, Specht T, Hinzmann B, Schmitt A, Pilarsky C, Dahl E;	
DR	WPI; 1999-591957/51.	
XX		
PT	New nucleic acid sequences expressed in uterine cancer tissues, and	
PT	derived polypeptides, for treatment of uterine and endometrial cancer	
XX	and identification of therapeutic agents	
XX		
PS	Claim 23; Page 287; 444pp; German.	
XX		
CC	This invention describes novel human nucleic acid (cDNA) sequences (A),	
CC	that are highly expressed in uterine tumour tissue and which have	
CC	anticancer and cytostatic activity. (A) are used (i) for recombinant	
CC	expression of polypeptides (B) and (ii) to isolate complete genes. (B)	
CC	are used (i) to identify agents suitable for treatment of uterine or	
CC	endometrial cancer; (ii) directly for treating these forms of cancer	
CC	(including expression from gene therapy vectors) and (iii) for	
CC	generation of specific antibodies. (A) are identified by assembling ESTs	
CC	(expressed sequence tags) from a particular tissue type before comparison	
CC	of expression patterns. This allows a significantly longer fragment of	
CC	the gene to be revealed, so should reduce the number of failures	
CC	associated with the fact that ESTs from different libraries may represent	
CC	different parts of the same unknown gene, distorting the estimated	
CC	frequency of occurrence in a particular tissue. AA59941-Y60328 represent	
CC	protein fragments encoded by the human endometrium tumour cDNA library	
CC	derived EST fragments represented in AA41981-742121.	
XX		
SO	Sequence 495 AA:	
XX		
Query Match	45.2%; Score 2491; DB 20; Length 495;	
Best Local Similarity	98.9%; Pred. No. 2.9e-187;	
Matches 461; Conservative	1; Mismatches 4; Indels 0; Gaps 0;	
OY	519 SRTNTPVETWKGSKGKOSTYIIIEENTTSFMAQRTFHEASRYTNDVAKIYSINVT	578
DB	1 SRTNTPVETWKGSKGKOSTYIIIEENTTSFMAQRTFHEASRYTNDVAKIYSINVT	60
OY	579 NVNMGVASYRCPCALEASDVSSGSCPCAGYIDRSGTCHSCPNTILKAHPYVOVQAC	638
DB	61 NVNMGVASYRCPCALEASDVSSGSCPCAGYIDRSGTCHSCPNTILKAHPYVOVQAC	120
OY	639 VPCPGTNNKTHSICYNDCFTSNTPTRFNFNSALANTVTLAGSPSTSGKLYFHH	698
DB	121 VPCPGTNNKTHSICYNDCFTSNTPTRFNFNSALANTVTLAGSPSTSGKLYFHH	180
OY	699 FTLSLGNQGRKMSVCTDNDLRIPGSGFSKITAAYCOAVIIPPEYTGKAGYSSQ	758
DB	181 FTLSLGNQGRKMSVCTDNDLRIPGSGFSKITAAYCOAVIIPPEYTGKAGYSSQ	240
OY	759 PVSILADRLIGVTTDMTLDGITSPALFHELSGIPDVIFEYFRSNDVQSCSSGRSTIRV	818
DB	241 PVSILADRLIGVTTDMTLDGITSPALFHELSGIPDVIFEYFRSNDVQSCSSGRSTIRV	300

QY 819 KCSPOKTVPGSLLPGETSGDTCDCNFHFLMESAAACPLCSVADYHAIVSSCVAGIOKT 878
 DB 301 KCSPOKTVPGSLLPGETSGDTCDCNFHFLMESAAACPLCSVADYHAIVSSCVAGIOKT 360
 QY 879 TVWMEPEPLCSGGISLPQRYVITCKTIDFWLKVGISAGTCTAILLVLTCEYFKKKNOKE 938
 DB 361 TVWMEPEPLCSGGISLPQRYVITCKTIDFWLKVGISAGTCTAILLVLTCEYFKKKNOKE 420
 QY 939 YKSKLVNNAATLKDCDLPADSCAIMGEDEVEDDLFTSKNHSIGR 984
 DB 421 YKSKLVNNAATLKDCDLPADSCAIMGEDEVEDDLFTSKNHSIGR 466

RESULT 11

ID AAB83853 standard; Protein; 383 AA.
 AC AAB83853;
 DT 23-JUL-2001 (first entry)
 DE Amino acid sequence of a human protein expressed in tumour cells.
 KW Tumour cell; immunological disease; autoimmune disease; cancer;
 KW infection.
 OS Homo sapiens.
 PN WO200131003-A1.
 PD 03-MAY-2001.
 PF 30-OCT-2000; 2000MO-FR03032.
 PR 29-OCT-1999; 99FR-0013629.
 PA (FABR) FABRE MEDICAMENT SA PIERRE.
 PI Delneste Y, Magistrelli G, Jeannin P, Bonnefoy J;
 DR WPI: 2001-328651/34.
 DR N-PSDB: AAF89777.
 PT New nucleic acid, expressed in tumours and lymphoid tissue is useful for
 PT identifying agents for treating tumours and autoimmune disease
 Claim 10: Page 74-75; 85pp; French.

The present sequence represents a human protein expressed in tumour cells. The polynucleotide is useful for screening cDNA/genomic DNA banks and for cloning isolated DNA; identifying mutant forms of the gene that encodes a human protein, where the mutations are associated with abnormal gene expression, or promoters and regulators of the gene, particularly for diagnosis; for recombinant expression of the gene, protein; as probes and primers for detection and amplification; and as antisense therapeutics. The tumour expressed protein is useful for activity, bind to it or interact with it. These agents are potentially useful for treatment or prevention of diseases associated with abnormal expression/activity of the protein, particularly immunological diseases (autoimmune diseases and cancer) or viral, bacterial, fungal or parasitic infections.

Sequence 383 AA.

Query Match 38.5%; Score 2119; DB 22: Length 383;
 Best Local Similarity 99.5%; Pred. No. 3.7e-158;
 Matches 381; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 136 SLSANNELDSDAESTGCTSKWPRDYLAFNTDECTATLMAVNLKOSGTVNFEEYY 195
 DB 1 SLSANNELDSDAESTGCTSKWPRDYLAFNTDECTATLMAVNLKOSGTVNFEEYY 60

QY 196 PDSSTIEEFVONQOCQPNADDSRMKTTTEKMEFHSVELNRGNVLYNRTAFSVMTKY 255
 DB 61 PDSSTIEEFVONQOCQPNADDSRMKTTTEKMEFHSVELNRGNVLYNRTAFSVMTKY 120
 QY 256 PKPVLVNRNIAITGVAATYSECEPCKPGTYADKQSSPFCKLCPASYSNKKETSCHOCDPK 315
 DB 121 PKPVLVNRNIAITGVAATYSECEPCKPGTYADKQSSPFCKLCPASYSNKKETSCHOCDPK 180
 QY 316 YSEKSSSCNRPACTCKDYFTHTACDANGETOLMYKNAKPKICSEDEGAVKLPASGV 375
 DB 181 YSEKSSSCNRPACTCKDYFTHTACDANGETOLMYKNAKPKICSEDEGAVKLPASGV 240
 QY 376 KTHCPNCPGFEFTYNNSTOCPCPYGSYNSGSDCTRCBPAGTEPAVGEYKMWATLPTNMT 435
 DB 241 KTHCPNCPGFEFTYNNSTOCPCPYGSYNSGSDCTRCBPAGTEPAVGEYKMWATLPTNMT 300
 QY 436 TVLSGTFEYKMGWGVADHITYTAAGASDNDPMLTLVVGFPFPOSVNADTEKRYA 495
 DB 301 TVLSGTFEYKMGWGVADHITYTAAGASDNDPMLTLVVGFPFPOSVNADTEKRYA 360
 QY 496 RITFEFETLCSVNCCELYFMVGVN 518
 DB 361 RITFEFETLCSVNCCELYFMVGVN 383

RESULT 12

ID AAB85768 standard; Protein; 372 AA.
 AC AAB85768;
 DT 29-OCT-2001 (first entry)

DE Human seven-transmembrane protein 50288 sequence.

seven-transmembrane protein; G-protein coupled receptor; GPCR; human;
 KW 17724; 50288; 31945; antiinflammatory; analgesic; cytosolic; virocidic;
 KW hepatotropic; immunosuppressive; gynecological; neuroprotective;
 KW anti-HIV; immunostimulant; dermatological; antiatherosclerotic; candidant;
 KW antianemic; antiParkinsonian; nephrotoxic; antithyroid; hemostatic;
 KW cerebroprotective; osteopathic; analgesic; gene therapy; nootropic.

OS Homo sapiens.
 PN WO200159117-A2.
 PD 16-AUG-2001.

PF 12-FEB-2001; 2001MO-US04536.
 PR 11-FEB-2000; 2000US-0182061.

PA (MILL-) MILLENNIUM PHARM INC.

PI Glucksmann MA, Silos-Santiago I;

DR WPI: 2001-514670/56.
 DR N-PSDB: AAH76195, AAH76196.

PT New seven-transmembrane protein/G-protein coupled receptor polypeptides
 PT and polynucleotides for diagnosing, treating seven-transmembrane
 PT protein/receptor-related disorders and to identify modulators of
 PT therapeutic use

Claim 8: Page 139-141; 144pp; English.

The invention provides isolated seven-transmembrane protein/G-protein coupled receptor polypeptides selected from 17724, 50288, 31945 proteins. Modulators of the polypeptides can be identified using a competition binding assay or an assay for receptor-mediated signal transduction. The polypeptides and polynucleotides are useful as reagents or targets in seven-transmembrane protein/receptor assays applicable to treatment and

diagnosis of seven-transmembrane protein/receptor-mediated disorders (see AAB48372 for a detailed description of the various disorders that can be treated or diagnosed using the polypeptides). The polynucleotides are useful to detect mutations in genes and gene expression products such as mRNA, as antisense constructs to control gene expression and for chromosome identification. The present sequence represents the human seven transmembrane protein 50288 sequence.

Sequence 372 AA:

Query Match 32.0%; Score 1761.5; DB 22; Length 372;

Best Local Similarity 96.7%; Pred. No. 4.8e-130; Indels 3; Gaps 1; Matches 318; Conservative 2; Mismatches 6;

1 MAEPGSHLSARVGRTERIPRLRLILWAGTAFOYTGCTGELHACKSEHYETA 60
1 MAEPGSHLSARVGRTERIPRLRLILWAGTAFOYTGCTGELHACKSEHYETA 60

61 CDSTGSRMVAVPHPTGLCTSLPDPVKGTECSFSCNAGEFLDMKQSCPCAEGRYSIGT 120
61 CDSTGSRMVAVPHPTGLCTSLPDPVKGTECSFSCNAGEFLDMKQSCPCAEGRYSIGT 120

121 GIPFDEDELPHGFASLSANMELDLSAESTGCTSSKVPBGDIATNTBCTATLMYA 180
121 GIPFDEDELPHGFASLSANMELDLSAESTGCTSSKVPBGDIATNTBCTATLMYA 180

121 GIPFDEDELPHGFASLSANMELDLSAESTGCTSSKVPBGDIATNTBCTATLMYA 180
121 GIPFDEDELPHGFASLSANMELDLSAESTGCTSSKVPBGDIATNTBCTATLMYA 180

181 VNKQSGTVNFEYYPDDSIIEFFVQNDCCPNADDSKMKTKRGMEFHSVELNRGN 240
181 VNKQSGTVNFEYYPDDSIIEFFVQNDCCPNADDSKMKTKRGMEFHSVELNRGN 240

241 VLYRTAFSVMTKVPKPVLRNIAITGVAYTSECPKPGYADKQSSFCFKLPANSY 300
241 VLYRTAFSVMTKVPKPVLRNIAITGVAYTSECPKPGYADKQSSFCFKLPANSY 300

301 SNKGETSCHOCDDPKYS---EKSSSCNV 326
301 SNKGETSCHOCDDPKYS---EKSSSCNV 326

301 SNKGETSCHOCDDPKYS---EKSSSCNV 326
301 SNKGETSCHOCDDPKYS---EKSSSCNV 326

301 SNKGETSCHOCDDPKYS---EKSSSCNV 326
301 SNKGETSCHOCDDPKYS---EKSSSCNV 326

301 SNKGETSCHOCDDPKYS---EKSSSCNV 326
301 SNKGETSCHOCDDPKYS---EKSSSCNV 326

Human SEC10 protein sequence (clone ID 1795045.0.77).

SECX: cytosolic; gynecological; gene therapy; screening assay; human;
SEC10: chromosomal mapping; forensic biology; cell proliferation; cancer;
cell differentiation; immune associated disorder; gestational disease.

Homo sapiens.
WO200078802-A2.

28-DEC-2000.
23-JUN-2000; 2000WO-US17328.

23-JUN-1999; 99US-0140584.
20-JUL-1999; 99US-0144722.
16-SEP-1999; 99US-0154520.
22-JUN-2000; 2000US-0604286.

(CURA-) CURAGEN CORP.

Shinkets RA, Fernandes E, Vernet C, Yang M, Boldog FL;
Herrmann JL;

WPI: 2001-071385/08.
N-PSDB; AAC84891.

polynucleotides encoding SECX proteins useful for treating disease characterized by an aberrant level of cell proliferation and/or differentiation like cancer or immune associated disorders -

Claim 1; Fig 10; 132pp; English.

The invention relates to human SECX polypeptides and polynucleotides encoding them. The SECX polypeptides can be expressed by standard recombinant methodology. The SECX polypeptides are useful in or preventing a SECX-associated disorder. The invention is useful in screening assays; detection assays (e.g. chromosomal mapping, cell and tissue typing, forensic biology); predictive medicine (diagnostic assays, prognostic assays, monitoring clinical trials, and pharmacogenomics); and methods of treatment (e.g. therapeutic and prophylactic), especially disorders characterized by aberrant cell proliferation and/or differentiation like cancer or immune associated disorders and/or disease. The present sequence represents a SEC10 protein.

Sequence 464 AA:

Query Match 26.3%; Score 1448; DB 22; Length 464;

Best Local Similarity 56.1%; Pred. No. 3.1e-105; Indels 6; Gaps 6; Matches 257; Conservative 73; Mismatches 122;

1 MKQVCSKCEGYSIGSGIKFDEMDELPAFSNIAFMDTVVGDSDRPGCNSSWIP 60
1 MKQVCSKCEGYSIGSGIKFDEMDELPAFSNIAFMDTVVGDSDRPGCNSSWIP 60

162 RGDIAFNDECTATLAVNINIKQSGTVNFEYYPDDSIIEFFVQNDCCPNADDSK 220
162 RGDIAFNDECTATLAVNINIKQSGTVNFEYYPDDSIIEFFVQNDCCPNADDSK 220

61 RGVIESNRDCVSLIYAVHLKSGYFEFFQYVQNNIEFFEFQNDCCQEMDTTDDK 120
61 RGVIESNRDCVSLIYAVHLKSGYFEFFQYVQNNIEFFEFQNDCCQEMDTTDDK 120

221 MKTEKG-WEFHSEYELNRGNVLYWRTAFSVTKVPKPVLRNIAITGVAYTSCFPCK 279
221 MKTEKG-WEFHSEYELNRGNVLYWRTAFSVTKVPKPVLRNIAITGVAYTSCFPCK 279

121 VKLTDNEMGSHVLMKSGTNIILYRTTGLIMSKAVKPVLYKNTIEBVAITSECFCK 180
121 VKLTDNEMGSHVLMKSGTNIILYRTTGLIMSKAVKPVLYKNTIEBVAITSECFCK 180

280 PGYADKQGSFCKLCPANSYSKGETSCHOC-DPPKYSSEKSSSCNVBPACTDKDYFT 338
280 PGYADKQGSFCKLCPANSYSKGETSCHOC-DPPKYSSEKSSSCNVBPACTDKDYFT 338

181 PGTFESNKRPGSFNCOVCPNRTYSEKAKECIRKDDDSFSESSSECTERPPCTTKDFOI 240
181 PGTFESNKRPGSFNCOVCPNRTYSEKAKECIRKDDDSFSESSSECTERPPCTTKDFOI 240

339 HTACDANGETOLMKWAKPKICSEDLGAVKLPASGVKTHCPGNGEFTNTNSQCPCK 398
339 HTACDANGETOLMKWAKPKICSEDLGAVKLPASGVKTHCPGNGEFTNTNSQCPCK 398

241 HTPCDEBKTOIMKWIPEKICREDLDAIRLPSEKCKPCPCNPGFYNSSCHPCP 300
241 HTPCDEBKTOIMKWIPEKICREDLDAIRLPSEKCKPCPCNPGFYNSSCHPCP 300

399 YGSYSNGS-DCTRCPCAGTEPAVGEYKWKWNTLPNTMETVLSGINFYKGMTGEVAGDH 457
399 YGSYSNGS-DCTRCPCAGTEPAVGEYKWKWNTLPNTMETVLSGINFYKGMTGEVAGDH 457

458 IYTAGASDNDPMILTVVPGFRPPOSVMADTENKEVARITFVEETLCSYNCLELYFWGV 517
458 IYTAGASDNDPMILTVVPGFRPPOSVMADTENKEVARITFVEETLCSYNCLELYFWGV 517

361 IOSGAGSDNDVLIILNHPKRPPTS-MTGATGSELRITFVEETLCSADCVLYFWVDI 419
361 IOSGAGSDNDVLIILNHPKRPPTS-MTGATGSELRITFVEETLCSADCVLYFWVDI 419

518 NSRINTPVETWKSGSKGOSTYIIEENTTSPTNAFOR 555
518 NSRINTPVETWKSGSKGOSTYIIEENTTSPTNAFOR 555

420 NRKSTNVESMGTKRKQAYTHIIFKNATFTWGIPIR 457
420 NRKSTNVESMGTKRKQAYTHIIFKNATFTWGIPIR 457

RESULT 14

AAB48372 standard; protein; 411 AA.

AAB48372; (first entry)

20-APR-2001 (first entry)

Human SEC5 protein sequence (clone ID 1795045.0.61).

SECX: cytosolic; gynecological; gene therapy; screening assay; human;
SEC5: chromosomal mapping; forensic biology; cell proliferation; cancer;
cell differentiation; immune associated disorder; gestational disease.
Homo sapiens.

XX WO200078802-A2.
 XX
 XX 28-DEC-2000.
 XX
 XX 23-JUN-2000; 2000WO-US17328.
 XX
 XX 23-JUN-1999; 99US-0140584.
 XX 20-JUL-1999; 99US-0144722.
 XX 16-SEP-1999; 99US-0154520.
 XX 22-JUN-2000; 2000US-0604286.
 XX
 XX (CURA-) CURAGEN CORP.
 XX
 PI Shimkets RA, Fernandes E, Vernet C, Yang M, Boldog FL;
 PI Hermann JL;
 DR MPI; 2001-071385/08.
 DR N-PSDB; AAC8486.
 XX
 XX Polynucleotides encoding SECX proteins useful for treating disease
 PT characterized by an aberrant level of cell proliferation and/or
 XX differentiation like cancer or immune associated disorders -
 XX
 XX Claim 1; Fig 6; 132pp; English.
 XX
 CC The invention relates to human SECX polypeptides and polynucleotides
 CC encoding them. The SECX polypeptides can be expressed by standard
 CC recombinant methodology. The SECX polypeptides are useful for treating
 CC or preventing a SECX-associated disorder. The invention is useful in
 CC screening assays; detection assays (e.g. chromosomal mapping, cell and
 CC tissue typing, forensic biology); predictive medicine (diagnostic assays,
 CC prognostic assays, monitoring clinical trials, and pharmacogenomics); and
 CC methods of treatment (e.g. therapeutic and prophylactic), especially
 CC disorders characterized by aberrant cell proliferation and/or
 CC differentiation like cancer or immune associated disorders or gestational
 CC disease. The present sequence represents a SEC5 protein.
 CC
 XX
 XX Sequence 411 AA;
 SQ
 Query Match 23.7%; Score 1307.5; DB 22; Length 411;
 Best Local Similarity 57.3%; Pred. No. 3e-94;
 Matches 231; Conservative 62; Mismatches 105; Indels 5; Gaps 5;
 QY 157 SKWPRGDIYAFNTDECTATIMYAVNLKSGTYVNFYDDSIIFEPVQDQOP-NA 215
 DB 3 SSMIPRCNTYIESNRDDCTSLIYAVHLKSGTYVNFYDDSIIFEPVQDQOQEMDT 62
 QY 216 DDSRMKTTKEG-WEPHSVELANGNVLYKRTTASVWTKVPVLYVRIATGVAATSE 274
 DB 63 TTDKRWKLDNGEMGSHVWLKSGTILYRTTGILMGSKAVKPVLYKNTIEGVAATSE 122
 QY 275 CFPCKRGTYADKOGSSFCALCPANSYNSKGETSCHOC-DPOKYSKSSSCNVRACIDK 333
 DB 123 CFPCKRGTFESNKRPGFNCQVCPRNTYSEKGAECIRCKDQSFSESGSECTERPPCTYK 182
 QY 334 DYFHTACDANGEOIAMKAKPKICSEDELGAVKLPASGVKHCPCNCGFEKTNST 393
 DB 183 DYQHTPCDEBERKTOIMKKEPICREDLDLDAIRLPSEKKKDCPCNCGFEKTNST 242
 QY 394 COPCPYGSYNSG-DOTRCPAGTEPAVGEFEYKMMNTLPTNNETVLSCINFEYKMGME 452
 DB 243 CHPCPGTGSDDGTCKRCPCPAGTEPALCFEYKMMNVLPGNKKTSCFVNGSKDCGNMGWE 302
 QY 453 VAGDHHTYTAGSDNDMILTLVPGFRPOSVADTENKEVARITFEFTLCSVNCLEY 512
 DB 303 VAGDHHTYTAGSDNDMILTLVPGFRPOSVADTENKEVARITFEFTLCSVNCLEY 361
 QY 513 FMVGVNSRTNTPVETWKSCKGOSTYIIEENTTSFTNAFOR 555
 DB 362 FMVGVNSRTNTPVETWKSCKGOSTYIIEENTTSFTNAFOR 404

RESULT 15
 AAB83852
 ID AAB83852 standard; Protein; 209 AA.
 XX
 XX AAB83852;
 AC
 XX 23-JUL-2001 (first entry)
 DT
 XX Amino acid sequence of a human protein expressed in tumour cells.
 DE
 XX Tumour cell; Immunological disease; autoimmune disease; cancer;
 KW
 KW Infection.
 KW
 OS Homo sapiens.
 XX
 XX WO200131003-A1.
 PN
 XX 03-MAY-2001.
 PD
 XX 30-OCT-2000; 2000WO-FR03032.
 PF
 XX 29-OCT-1999; 99FR-0013629.
 PR
 XX (FABR) FABRE MEDICAMENT SA PIERRE.
 PA
 XX Delneste Y, Magistrelli G, Jeannin P, Bonnefoy J;
 PI MPI; 2001-328651/34.
 DR N-PSDB; AAF89776.
 DR
 XX New nucleic acid, expressed in tumours and lymphoid tissue is useful for
 PT identifying agents for treating tumours and autoimmune disease -
 PT
 XX Claim 10; Page 71-72; 85pp; French.
 PS
 XX
 CC The present sequence represents a human protein expressed in tumour
 CC cells. The polynucleotide is useful for screening cDNA/genomic DNA banks
 CC and for cloning isolated DNA, identifying mutant forms of the gene that
 CC encodes a human protein, where the mutations are associated with
 CC abnormal gene expression, or promoters and regulators of the gene,
 CC particularly for diagnosis; for recombinant expression of the derived
 CC protein; as probes and primers for detection and amplification; and
 CC as antisense therapeutics. The tumour expressed protein is useful for
 CC raising specific antibodies. The tumour expressed protein is useful for
 CC activity, bind to it or interact with it. These agents are potentially
 CC useful for treatment or prevention of diseases associated with abnormal
 CC expression/activity of the protein, particularly immunological diseases
 CC (autoimmune diseases and cancer) or viral, bacterial, fungal or parasitic
 CC infections.
 CC
 XX
 XX Sequence 209 AA;
 SQ
 Query Match 21.2%; Score 1169; DB 22; Length 209;
 Best Local Similarity 99.5%; Pred. No. 8.8e-84;
 Matches 208; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 310 QCDPKYSEKSSSCNVRPACTDKDYFTHACDANGERTOLMYAPKICSEDLBAVK 369
 DB 1 QCDPKYSEKSSSCNVRPACTDKDYFTHACDANGERTOLMYAPKICSEDLBAVK 60
 QY 370 LPASGVKTHCPNCGFEKTNSTCQPCPYGSYNSGSDCTRCPAGTEPAVGEYKMMNTL 429
 DB 61 LPASGVKTHCPNCGFEKTNSTCQPCPYGSYNSGSDCTRCPAGTEPAVGEYKMMNTL 120
 QY 430 PTNMTETVLSCINFEYKMGMEVAGDHIYTAAGASNDMILTLVPGFRPOSVMAOT 489
 DB 121 PTNMTETVLSCINFEYKMGMEVAGDHIYTAAGASNDMILTLVPGFRPOSVMAOT 180
 QY 490 ENKEVARITFEFTLCSVNCLEYFMVGVN 518
 DB 181 ENKEVARITFEFTLCSVNCLEYFMVGVN 209

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Page 13

Search completed: March 12, 2003, 00:12:51
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